

GenBank (c) 1998-2002 by National Center for Human Genome Research, Inc.

Search using SWISS-PROT

18 Jul 2002, 23:10:33 Search time 2673.95 Seconds
(without alignments)
4108690 Million cell updates/sec

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us-09-254-760a-18

10:27:32 2002

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Search, using SW and/or

on 10/27/2002, 00:43:56. Search time 377.69 seconds

(without alignments)
2,566,561 Million cell updates/sec

us-09-254-760a-18

Protein data bank (PDB) accession number: 525

ENZYME NO:

EC NO: 3.5.1.1

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and by analysis of the results above distribution.

SUMMARY

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AAV29048	525	Human ovarian tumo
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AAV29048	525	Human XAG growth f
AAV29048	525	Human huxag-1/500G
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FW	immunomodulatory; anti-inflammatory; inhibitory
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FT	/stat
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PF	12-SEP-1997
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PP	12-SEP-1997
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PA	(PROT) PROLEPTIN IN"

23-AUG-1996; 96W0-US13766.
(HUMAN) HUMAN GROWTH FACTOR 1 (HGF)
Dillon PJ, Ebner R, Andrews GA, Yu G;
WPI; 1998-169093/15.
P-PSDB; AAW37844.
New isolated human XAG growth factor(s) used to develop products for treating e.g. liver, lung or breast diseases or hyperproliferative disorders, e.g. cancer.
Claim 5; Fig 1; 14pp; English.
This cDNA clone codes for huXAG-1 (see AAW37844), a member of a novel family of human growth factors also including huXAG 2 (see AAW37845) and huXAG 3 (see AAW37846). These proteins share homology with the XAG protein of *Xenopus laevis*, which is involved in embryogenesis and is expressed in adult tissue. Expression of huXAG 1 has been demonstrated in skin, nerve, muscle, with a corresponding expression in healthy colon tissue. The huXAG-1 gene, also designated colon cancer-specific gene (CCSG), provides a molecular marker for colon cancer. huXAG-1 cDNA was isolated from a cDNA library derived from human colon cancer tissue. Vectors, host cells, antibodies, and screening methods for identifying agonists and antagonists of huXAG 1 are provided. huXAG polypeptides are growth factors and can be used to stimulate proliferation of cells. They can be used to stimulate the proliferation and differentiation of hepatocytes to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances. They can also be used to stimulate or promote liver regeneration, e.g. after surgery. They can also be used to prevent and heal damage to the lungs caused by various pathological states. They can be used to stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent, attenuate, or treat acute or chronic lung damage, e.g. emphysema, which results in the progressive loss of alveoli, and inhalation injuries, e.g. resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli. They can also be used to stimulate the proliferation and differentiation of breast tissue and could therefore be used to promote healing of breast tissue injury due to surgery, trauma or cancer. Antagonists can be used to treat hyperproliferative disorders, including cancer, in particular hepatocellular carcinoma, osteosarcoma, breast cancer, or colon cancer. The products can also be used for detection and diagnosis.

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Best Local Similarity	99.88;	pred. No.	2.5e-142;		
Matches	524;	conservation	6;	alignability	11;
				Index	6;
				Gap	67;

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[illegible]

Novel human growth factor polypeptide useful for diagnosing and treating colon cancer and liver diseases, to prevent and treat damage to the lungs and for identifying modulators of therapeutic usage -

PZ claim 4^b; Pz 1; Applicant's

This invention relates to a human growth factor polypeptide, huXAG, also known as a colon cancer specific gene (CCSG), huXAG-1, as an inhibitor of proliferation as a growth factor, the huXAG-1 protein is useful for identifying compounds capable of enhancing or inhibiting cellular response induced by huXAG-1, the protein is also useful for stimulating proliferation of cells e.g., colon, breast, liver and pancreatic and hepatocytes. It is useful for alleviating or treating liver diseases and pathologies such as malignant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances, for preventing and treating damage to the lungs caused by various pathological states and for promoting healing of breast tissue injury due to surgery. Further, cancer, huXAG-1 and the identified antagonist are useful for treating cancer, in particular, colon cancer, to detect elevated levels of huXAG-1 and its polypeptides are useful for diagnosing or detecting cancer in mammals. The gene encoding huXAG-1 is useful for medical diagnosis.

[illegible]

oy 481 ct t q u a c a t q a q u a d e t c t c a n t t c t q a q a 517
| | | | | | | | | | | | | | | |
pb 533 c t t q a r - c a t q a u a a d e t c t c a n t t c t r a d a 567

Search completed: July 19, 2002, 03:38:57
Job time: 10519 sec

Sequence 1, Application US/09916376B
Patent No. 6171816
GENERAL INFORMATION:
APPLICANT: YU, GHO LIANG
APPLICANT: BULLON, PATRICK J.
APPLICANT: BENNER, REINHARD
APPLICANT: ENKRESS, GREGORY A.
APPLICANT: LAMM, ROYAL HUBAN GROWTH FACTORS
NUMBER OF SEQUENCES: 45
CURRENT ADDRESS ADDRESS:
ADDRESS: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-0934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/09916376B
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 617024147
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFF, ERIC K.
REGISTRATION NUMBER: 46,688
REFERENCE/DOCKET NUMBER: 1488,0500001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 471-2660
TELEFAX: (202) 471-2640
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 71..595
NAME/KEY: mat_peptide
LOCATION: 131..595

ALIGNMENTS

RESULT 1
US-08 916-575B 1
Sequence 1, Application US/09916376B
Patent No. 6171816
GENERAL INFORMATION:
APPLICANT: YU, GHO LIANG
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APPLICANT: ENKRESS, GREGORY A.
APPLICANT: LAMM, ROYAL HUBAN GROWTH FACTORS
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ZIP: 20005-0934
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
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NAME: STEFF, ERIC K.
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REFERENCE/DOCKET NUMBER: 1488,0500001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 471-2660
TELEFAX: (202) 471-2640
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 71..595
NAME/KEY: mat_peptide
LOCATION: 131..595

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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NAME/KEY: CDS
LOCATION: 71..595
NAME/KEY: mat_peptide
LOCATION: 131..595

ALIGNMENTS

RESULT 1
US-08 916-575B 1
Sequence 1, Application US/09916376B
Patent No. 6171816
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
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TOPOLOGY: linear
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FEATURE:
NAME/KEY: CDS
LOCATION: 71..595
NAME/KEY: mat_peptide
LOCATION: 131..595

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and by analysis of the total score distribution.

SUMMARY

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3	875	3	Sequence 149, App
4	875	4	Sequence 78, Appl
5	875	5	Sequence 78, Appl
6	875	6	Sequence 32, Appl
7	875	7	Sequence 35, Appl
8	875	8	Sequence 9, Appl
9	875	9	Sequence 36, Appl
10	875	10	Sequence 10, Appl
11	875	11	Sequence 5, Appl
12	875	12	Sequence 209, App
13	875	13	Sequence 37, Appl
14	875	14	Sequence 11, Appl
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17	875	17	Sequence 14, Appl
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 : GENERAL INFORMATION:
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 : APPLICANT: Wang, Tonglong
 : TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
 : FILE REFERENCE: 21012145521
 : CURRENT APPLICATION NUMBER: US/09123,912A
 : CURRENT FILING DATE: 1998 07 27
 : PRIOR APPLICATION NUMBER: 09/040,802
 : PRIOR FILING DATE: 1998-03 18
 : NUMBER OF SEQ ID NOS: 114
 : SOFTWARE: PatentIn Ver. 2.0
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 : ORGANISM: Homo sapiens
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 : LOCATION: (787)
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 : Patent No. 6284241
 : GENERAL INFORMATION:
 : APPLICANT: X0, dunnellum
 : TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
 : FILE REFERENCE: 210121471
 : CURRENT APPLICATION NUMBER: US/092212298
 : CURRENT FILING DATE: 1998-12-23
 : NUMBER OF SEQ ID NOS: 112
 : SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
 : SEQ ID NO 32
 : LENGTH: 401
 : TYPE: DNA
 : ORGANISM: Human
 US-09-221-298-32

Query Match 72.9% Score 201.10 DB 475 Length 480
 Best Local Similarity 99.5% Prod. No. 6312695
 Matches 199 Conservative 0 Mismatches 11

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,607
FILING DATE: 25 FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kaki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/CKET NUMBER: 210121.42703
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 159 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-040-607-209

Query Match: 25.4%; Error: 136; Obj 1, Length: 153;
Best Local Similarity: 100.0%; Prod. No.: 18034;
Matches: 136; Conservation: 0; Mismatch: 0; Indel: 0

[illegible]

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RESULT 33
US-09-459 313-209
? 2009-09-29, Applicant in 2009-09-29
? Patent No. 6329505
? GENERAL INFORMATION:
? APPLICANT: Xu, Jiangchun
? APPLICANT: Patten, David G.
? APPLICANT: Mischum, Jennifer L.
? APPLICANT: Harlocker, Susan Louise
? APPLICANT: Jiang Yuqi
? APPLICANT: Reed, Steven G.
? APPLICANT: Kates, Michael
? APPLICANT: Pander, Gary
? APPLICANT: Ketter, Mark
? APPLICANT: Solik, John
? APPLICANT: Dry, Craig
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF PROSTATIC CANCER
? FILE REFERENCE: 21612142789
? CURRENT APPLICATION NUMBER: 09/994439, 313
? CURRENT FILING DATE: 1999 11-12
? NUMBER OF SEQ ID NOS: 575
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 209
? LENGTH: 159

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; TYPE: DNA
 ; ORGANISM: Homo sapien
 [J03044:439-473:209]

US 44-434-373 2004

[illegible]

RECEIVED 14
 MS-08-016 576B 37
 , 3640000 17, 6741000 657000 65764
 , 64000 6741000

GENERAL INFORMATION:
APPLICANT: YU, GIDU LIANG
APPLICANT: ELLIOT, PATRICK E.
APPLICANT: EMMER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NAVEL REMOVAL WITH EXTRACTS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNEL, KIRSNER & F. X. FLEISCH
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC

```

1 COUNTRY: US
2 ZIP: 23030-3934
3 COMPUTER RELEASABLE PROGRAM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC DOS/MS DOS
7 SOFTWARE: Patent Pending # 4,111,763
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/947,576B

```

CLASSIFICATION: 546
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 371-2640
FILING DATE: 23 AUG 1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFF, ERIC K.
REGISTRATION NUMBER: 367,688
REFERENCE/EXCERPT NUMBER: 1189, 1000, 1001
TECHNICAL INFORMATION:
TELEPHONE: (202) 371-2640
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 base pairs
TYPE: nucleic acid
TRANSLATION: simple
TOPOLOGY: linear
MULTIPLE TYPE: CDS
LOCUS: 371-2640.37

Quarry Match 19, 48; Score 10.1; Lfs 4; Length 1.52;
Best Local Similarity 100%; Prod. No. 1,462;
Matches 10; Conservation 0; MisMatches 0; Index 100; Error

[illegible][illegible]



Db 658 ATGACTGAGAGATATTAAAGGCTCTCTATATCTTACGAACCTTCATATACAGCTCTCTGTTG 599
QY 481 ctttacaacatgaagaaatctctcaatttgcctgaagactgaattt 525
Db 598 CTTGACAAACATGAAGAAAGCTCTCAAGCTGCTCAAGACTGAATTCG 554

RESULT 5
PCT-US00-25524B-2108
Sequence 2108, Application PG/1000006524B
GENERAL INFORMATION:
APPLICANT: Elise et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polypeptides and Polypeptide
FILE REFERENCE: PA095PCT
CURRENT APPLICATION NUMBER: 100/000006524B
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,109
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,290
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ IDS NOS: 8564
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2108
LENGTH: 943
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (866)
OTHER INFORMATION: n equals a,t,g, or c
PCT-US00-25524B-2108

Query Match 99.9%; Score 524.6; DB 1; Length 943;
Best Local Similarity 99.9%; Pred. No. 439; 149;
Matches 524; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgagagaaatttcatttcacatttgcctcttgcctctctctcactctgcct 60
Db 83 atgagagaaatttcatttcacatttgcctcttgcctctctctcactctgcct 142
QY 61 agagataccacagtcagaaatctgaagaaacacaaagaaatctctgaacaaactg 120
Db 143 agagataccacagtcagaaatctgaagaaacacaaagaaatctctgaacaaactg 202
QY 121 ccccaacacacctctctcagagtttgcctctctcagagttctcagagttctcagagtt 180
Db 203 ccccaacacacctctctcagagtttgcctctctcagagttctcagagttctcagagtt 262
QY 181 gct 240
Db 263 gct 322
QY 241 tgcacacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 300
Db 323 tgcacacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 382
QY 301 gcaagacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 360
Db 383 gcaagacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 442
QY 361 gct 420
Db 443 gct 502
QY 421 atcactgaagatattcagagctctctcagagctctctcagagctctctcagagctctctcagag 480
Db 503 atcactgaagatattcagagctctctcagagctctctcagagctctctcagagctctctcagag 562
QY 481 ctttacaacatgaagaaatctctcaatttgcctgaagactgaattt 525

Db 563 ctttacaacatgaagaaatctctcaatttgcctgaagactgaattt 525
RESULT 6
US-09-792-439-1
Sequence 1, Application US/09792439
GENERAL INFORMATION:
APPLICANT: Boyd, Robert Simon
APPLICANT: Gump, Alasdair Craig
APPLICANT: Jernett, Jonathan Alexander
APPLICANT: Jyson, Kerry Louise
TITLE OF INVENTION: Polypeptides and Therapeutic Methods
FILE REFERENCE: 25431005N
CURRENT APPLICATION NUMBER: 09/792439
CURRENT FILING DATE: 2001-02-23
PCT-A PUBLICATION NUMBER: GB 000457635
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ IDS NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 543
TYPE: DNA
ORGANISM: human
US-09-792-439-1

Query Match 99.7%; Score 524.3; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 870; 149;
Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgagaaatcccaatctcagactctctgcctctctgcctctctgcctctctgcctctctgcctct 40
Db 11 atgagaaatcccaatctcagactctctgcctctctgcctctctgcctctctgcctctctgcctct 80
QY 61 aaagataccacagtcagaaatctgaagaaacacaaagaaatctctgaacaaactctgaacaaact 120
Db 73 aaagataccacagtcagaaatctgaagaaacacaaagaaatctctgaacaaactctgaacaaact 180
QY 121 ccccaacacacctctctcagagtttgcctctctcagagttctcagagttctcagagttctcagagtt 180
Db 131 ccccaacacacctctctcagagtttgcctctctcagagttctcagagttctcagagttctcagagtt 240
QY 181 gct 240
Db 191 gct 300
QY 241 tgcacacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 300
Db 251 tgcacacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 360
QY 301 gcaagacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 360
Db 311 gcaagacacagtcagaaatcttgaagaaatcttgaagaaatcttgaagaaatcttgaagaaat 420
QY 361 gct 420
Db 371 gct 480
QY 421 atcactgaagatattcagagctctctcagagctctctcagagctctctcagagctctctcagag 480
Db 431 atcactgaagatattcagagctctctcagagctctctcagagctctctcagagctctctcagag 540
QY 481 ctttacaacatgaagaaatctctcaatttgcctgaagactgaattt 520
Db 491 ctttacaacatgaagaaatctctcaatttgcctgaagactgaattt 580

RESULT 7
PCT-US02-02470-1140
Sequence 1140, Application PG/1000002870
GENERAL INFORMATION:
APPLICANT: Elise et al.

[illegible]

Figure 1. The effect of the concentration of the H_2O_2 solution on the amount of the released H_2 gas from the H_2 gas-generating system. The amount of the released H_2 gas was measured at 25 °C for 10 min. The concentration of the H_2O_2 solution was 0.01, 0.02, 0.05, 0.1, 0.2, 0.5, 1, 2, 5, 10, 20, 50, 100, 200, 500, 1000, and 2000 ppm. The amount of the released H_2 gas was measured at 25 °C for 10 min. The concentration of the H_2O_2 solution was 0.01, 0.02, 0.05, 0.1, 0.2, 0.5, 1, 2, 5, 10, 20, 50, 100, 200, 500, 1000, and 2000 ppm.



QY	301	qeaqqaaqt t t q e c t e e t c a a t e t q u f f l a t q a a r c a d e t q a c a a c a c o t t e c c e t	360
Dd	301	qeaqqaaqt t t q e c t e e t c a a t e t q u f f l a t q a a r c a d e t q a c a a c a c o t t e c c e t	360
QY	361	qat qe c c a a t a t q t e e c c a q u a t t a t a t t q t t q a c c a t e t e t q a c a t t a q a a c c a t	420
Dd	361	qat qe c c a a t a t q t e e c c a q u a t t a t a t t q t t q a c c a t e t e t q a c a t t a q a a c c a t	420
QY	421	a t c a c t q u a g a t a t t e a a a r e q t e t e t a t q e t t a n q a a c e t q a a t a t a c a q e t e t q t t q	480
Dd	421	a t c a c t q u a g a t a t t e a a a r e q t e t e t a t q e t t a n q a a c e t q a a t a t a c a q e t e t q t t q	480
QY	481	e t t q a a c a t q a a q a a a q t e t e c a a q t k p e t q a a q a t q a a t t q	525
Dd	481	e t t q a a c a t q a a q a a a q t e t e c a a q t k p e t q a a q a t q a a t t q	525

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RESULT      2
US 09-254 760A 27
; SEQ ID NO : 27; Application No.: 09-254 760A
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANTS: Sekino, Shingo
; APPLICANTS: Kimura, Tomoya
; APPLICANTS: Kobayashi, Midori
; TITLE OF INVENTION: HUMAN PROTEIN HAVING PROPERTY FOR
; TITLE OF INVENTION: SEQUENCES AND DNAs ENCODING THESE PROTEINS
; FILE REFERENCE: GIN-6704/prots
; CURRENT APPLICATION NUMBER: US/09/254,760A
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: JP 8/243,060
; PRIOR FILING DATE: 1996-09-13
; PCT APPLICATION NUMBER: PCT/JP97/00300
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO : 27
; LENGTH: 866
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(597)
US 09-254 760A-27

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[illegible]

bb 373 qeapqaeaaat t t q t c t c t e a t e t q t t t t t q a q a d e t q a c a a q e e t t a t c e t t 373

QY 361 qat qeaaat a t a t e e c a a a t t a t q t t t t t q a c e a t e t q a a t t a d a a c a t 361

bb 433 tat qeaaat a t a t e e c a a a t t a t t t t q a c e a t e t q a a t t a d a a c a t 366

QY 421 at e a c t q a a a t a t t e a a a q e e t e t a t q t t a a a q e e t q a a t a c a t e t q t t a 421

bb 493 at e a c t a a a a t a t t e a a a q e e t e t a t q t t a a a q e e t q a a t t a d a a c a t 493

QY 481 e t t q a a q e e t q a a a a a t t e t e a a t t t a t a a q a a t t a t 481

bb 563 e t t q a a q e e t q a a a a a t t e t e a a t t t a t a a q a a t t a t 563

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RESULT: 3
US 10 106-698-2118
; Sequence 2118, Application US/10106-698
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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; ADDRESS: 106-698-2118 and 106-698-2118
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10106-698
; CURRENT FILING DATE: 2002-09-27
; PRIORITY APPLICATION NUMBER: US/000000/26624
; PRIORITY FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/00/107,147
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US/00/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patent In Ver. 3.0
; SEQ ID No 2118
;
; FEATURE: 54
; TYPE: DNA
;
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: equals 2118, of 8
; NAME/KEY: misc feature
; LOCATION: (866)..(866)
; OTHER INFORMATION: equals 2118, of 8
US 10 106-698-2118

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[illegible]

Search completed: July 19, 2002, 04:44:44
Job time: 1426 Sec

RESULTS

Query Match	76.38;	Score 400.6;	DB 6;	Length 535;
Best Local Similarity	99.0%;	Pred. No. 1.6e-11;		
Matches 403;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

us-09-254-760a-18.rnpn

0:27:33 2002

Fri



DNA Sequencing by: Inocyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the T.M.A.C.E. Consortium/URL at:
<http://image.tma.gov>
 Plate: L1AM1574 row: h column: 04
 High quality sequence start: 5
 High quality sequence stop: 624.
 Location/Qualities
 1..624
 +organism "Homo sapiens"
 /db_xref "taxon:9606"
 /clone IMAGE:5201341
 /clone_11E "NHL_MGC_122"
 /lab_host "DH10B"
 /note "Strain: pooled lung and spleen; Vector: pCMV-SGR167
 Site_1: Not1; Site_2: EcoRV (destroyed); RNA source:
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleen. Library is cDNA, 3'
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Geneticon tracking code 020. Note:
 this is a NHL MGC Library."

[illegible]

mRNA sequences.
R0778248
R0778249
EST:
Location:
Human.
Organism:
Homo Sapiens
Eukaryote; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
1 (bases 1 to 66)
RefSeq: [NM_001122043.2](#)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.,
Email: [carpenter@mail.nih.gov](#)
Tissue Procurement: [PMT/DTP](#)
cDNA Library Preparation: [GenScript High Pure Tissues](#), Inc.
cDNA Library Arrayed by: The L.M.A.C.E. Consortium (LNC)
Data Sequencing by: Invitrogenomics, Inc.
Clone Distribution: Mac clone distribution information can be
found through the L.M.A.C.E. Consortium/LINC at:
[http://www.linc.org](#)
Plate: LAM1656, row: 1 column: 36
High quality sequence stop: 665,
Location/Zenith:

[illegible]

10:27:33 2002

Fri





29 SEP-1999: 99US-0157157.
03 NOV-1999: 99US-0163280.
(HUMAN) HUMAN GENOME SCI. 1901.
Ruben SM, Barash SC, Bitse CP, Rosen CA.
WPI: 2001-245257/24.
P-PSDB: AAG75621.
Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
useful for preventing, diagnosing and/or treating colorectal cancers
Claim 1; Page 3593; 9803pp; English.
AAH32943 to AAH37195 and AAG75514 to AAG77789 represent human colon
cancer-associated nucleic acid molecules (N) and proteins (P), where
the proteins are collectively known as colon cancer antigens. The colon
cancer antigens have cytostatic activity and can be used in gene
therapy and vaccine production. N and P may be used in the prevention,
diagnosis and treatment of diseases associated with inappropriate P
expression. For example, N and P may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of P by expressing
inactive proteins or to supplement the patient's own production of P.
Additionally, N may be used to produce the colon cancer-associated Ps,
by inserting the nucleic acids into a host cell and culturing the cell
to express the proteins. N and P can be used in the prevention, diagnosis
and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
and AAG77789 represent sequences used in the exemplification of the
present invention.
N.B. Pages 666 to 682 and page 7053 of the sequence listing were
missing at time of publication, meaning no sequences are present for
SEQ ID NO:1027 to 1052, 7921 and 7922.
Sequence 943 BP; 311 A; 199 G; 199 G; 229 T; 5 others;

[illegible][illegible]


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US 08 916 576B
: Sequence 5, Application US/08916576B
: Patent No. 6171816
: GENERAL INFORMATION:
: APPLICANT: YG GENIUM
: APPLICANT: DILLON, PATRICK J.
: APPLICANT: EHRER, REINHARD
: APPLICANT: ENDRESS, GREGORY A.
: TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESTER, GORSTIN & FOX, P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, Suite 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: US
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS DOS
: SOFTWARE: Patent In License #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/916,576B
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/024,347
: FILING DATE: 23 AUG 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: STEFF, ERIC K.
: REGISTRATION NUMBER: 36,699
: REFERENCE/DECKET NUMBER: 1488,050061
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 732 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 49..546
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 49..117
:
US 08 916 576B-5

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[illegible][illegible][illegible]

TELECOMMUNICATION INFORMATION;
TELEPHONE: (202) 471-2600
TELEFAX: (202) 471-2540
INTERNET FOR GRC: <http://www.gcr.gov>
SEQUENCE CHARACTERISTICS;
LENGTH: 136 base pairs
TYPE: nucleic acid
STRANDELNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-0416-5763-38

Query Match	12.9%	Score	112	DB 4	Length	136			
Best Local Similarity	98.5%	Pred. No.	2.1e-23						
Matches	134	Conservative	0	Mismatches	0	Indels	27	Gaps	27

[illegible][illegible]

Qy	146	qat	acacacatt	caaac	151
Ub	120	GATAC	TACAGTCAAC		135

Search completed: July 19, 2002, 02:12:29
Job time: 9056 sec

GenBank accession number: U00001.1

Query: us-09-254-760a-27

Query: us-09-254-760a-27
Query: us-09-254-760a-27
Query: us-09-254-760a-27

us-09-254-760a-27

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us-09-254-760a-27


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; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO: 1
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/TYPE: CDS-coding
; OTHER INFORMATION: CDS1
; OS: 09/981-353591

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Query Match	99.89%	Score: 964.4	199.46	Length: 1000
Best Local Similarity	99.98%	Prod. No. 6.9e-21		
Matches: 965	Conservative	97 Mismatches	17 Indels	0

[illegible]

SEARCHED INDEXED
SERIALIZED FILED
FBI - NEW YORK
JUN 14 2002
FBI - NEW YORK

RECEIVED FROM THE FBI - NEW YORK

DATE: 6/14/2002

TIME: 10:27:35
FROM: NEW YORK
TO: NEW YORK

RE: [REDACTED]

DATE: 6/14/2002

TIME: 10:27:35

FROM: NEW YORK

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FROM: NEW YORK

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DATE: 6/14/2002

TIME: 10:27:35

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us-09-254-760a-27.rnrm
Page 7

SEARCHED INDEXED
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JUN 14 2002
FBI - NEW YORK

RECEIVED FROM THE FBI - NEW YORK

DATE: 6/14/2002

TIME: 10:27:35

FROM: NEW YORK

TO: NEW YORK

RE: [REDACTED]

DATE: 6/14/2002

TIME: 10:27:35

FROM: NEW YORK

TO: NEW YORK

RE: [REDACTED]

DATE: 6/14/2002

TIME: 10:27:35

FROM: NEW YORK

TO: NEW YORK

RE: [REDACTED]

DATE: 6/14/2002

TIME: 10:27:35

FROM: NEW YORK

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TIME: 10:27:35

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DATE: 6/14/2002

TIME: 10:27:35

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RE: [REDACTED]

DATE: 6/14/2002

TIME: 10:27:35

FROM: NEW YORK

TO: NEW YORK

RE: [REDACTED]

DATE: 6/14/2002

TIME: 10:27:35

FROM: NEW YORK

TO: NEW YORK

RE: [REDACTED]

DATE: 6/14/2002

TIME: 10:27:35

Seq 84: 101110000000000000000000
 111111111111111111111111
 Obj 908 101110000000000000000000

RESULT 15
 OS-09-47: 276, 10277
 : Sequence 1027, Application OS/094 / 1275
 : GENERAL INFORMATION:
 : APPLICANT: HYSEON, LLC.

RESULTS 15
05-09-47: 275, 1027/s
; Sequence 1027, Amplification: 35/34/1275

```

1  APPLICANT:  HYSECO, INC.
2
3  TITLE OF INVENTION:  Novel Composites of Fibers
4  TITLE OF INVENTION:  From Various Libraries
5
6  FILE REFERENCE:  782
7
8  CURRENT APPLICATION NUMBER:  09/247,276
9
10 CURRENT FILING DATE:  1999-12-23
11
12 EARLIER APPLICATION NUMBER:  09/255,076
13 EARLIER FILING DATE:  1999-01-20
14
15 EARLIER APPLICATION NUMBER:  09/254,661
16 EARLIER FILING DATE:  1999-01-22
17
18 EARLIER APPLICATION NUMBER:  09/246,671
19 EARLIER FILING DATE:  1999-01-29
20
21 EARLIER APPLICATION NUMBER:  09/277,227
22 EARLIER FILING DATE:  1999-03-25
23
24 EARLIER APPLICATION NUMBER:  09/277,499
25 EARLIER FILING DATE:  1999-03-18
26
27 EARLIER APPLICATION NUMBER:  09/277,972
28 EARLIER FILING DATE:  1999-04-16
29
30 EARLIER APPLICATION NUMBER:  09/274,861
31 EARLIER FILING DATE:  1999-03-24
32
33 EARLIER APPLICATION NUMBER:  09/272,463

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Quercy Mat'el.	96.12%	26.70 and 4.18 1900	1000 ft. 1900
Best local Similarity	99.98%	Prod. No. 4,500 2199	
Matched R50: Conser valve	0	Mismatching	1
			1000 2199

[illegible]



Fri Jul 19 10:27:35 2002

us-09-254-760a-27.rnpn

Page 10

[illegible]

CC response, signal sequences from the cDNAs can be used in construction of
CC secretion vectors; other sequences derived from the extended cDNAs can be
CC used to clone upstream genomic DNA sequences including promoters. This is
CC in turn useful for identifying proteins that interact with promoter
CC sequences. Some of the proteins may be useful in diagnosing and treating
CC several disorders including, but not limited to: cancer, hyperlipidaemia,
CC cardiovascular and neurodegenerative disorders, autoimmune diseases, and
CC rheumatic diseases, embryonic disorders, hypertension, renal injury,
CC amino acidurias, hypoglycaemia, male rat infertility and myopathies.

XX Sequence 131 AA;

Query Match 67.3% Score 605; DB 20; Length 141;
Best local similarity 92.9% PID: 304.30.5%
Matches 11%; Conservation 0% Mismatches 9% Indels 0% Gaps 0%

QY 1 MPEFIVYALIVVALVYIAKLVVPI 244; 100% coverage of the WT sequence
DB 1 MPEFIVYALIVVALVYIAKLVVPI 244; 100% coverage of the WT sequence
QY 61 AAYFSEFQNPIMMHHHFFRRH2ALFFVFAREH2ELZLFVAINVYHITZELCP 120
DB 61 AAYFSEFQNPIMMHHHFFRRH2ALFFVFAREH2ELZLFVAINVYHITZELCP 120
QY 121 DGQYVP 126
DB 121 DGQYVP 126

RESULT 13

AAV12312
ID AAY12312 standard; Protein: 116 AA;

XX AAY12312;

DE 17 JUN 1999 (first entry)

DE Human 5' EST secreted protein SEQ ID NO:343.

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW torensin; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; hematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokine; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.

XX Homo sapiens.

XX W0906548-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 58W0-180122.

XX 01-AUG-1997; 9705-0905145.

XX (GENSET) GENSET.

XX Lucifert A.; Thomas Milne Edwards J.; Lucifert B.

XX WPI: 1999-192779/17.

XX N PSDB: AAX41145.

XX New nucleic acids encoding human secreted proteins - obtained from
PI cDNA libraries prepared from testis, liver, ovary, brain, prostate,
PI kidney, lung, umbilical cord, placenta and colon tissue

XX claim 27; Page 682; 824pp; English.

XX AAX41094 to AAX41147 represent 3' expressed sequence tags (ESTs) for
CC human secreted proteins) and encode the proteins given in AAY12261 to
CC AAY12514, respectively. The proteins given represent the signal peptide

CC and an N terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulation
CC activity, tissue growth regulation activity, reproductive hormone
CC regulation activity, haemostatic/chemotactic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in torensin, gene therapy and chromosome mapping products.
CC the sequences can also be used for obtaining corresponding protein
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell

XX Sequence 116 AA;

Query Match 66.5% Score 606; DB 20; Length 116;
Best local similarity 100.0% PID: 304.30.5%
Matches 11%; Conservation 0% Mismatches 0% Indels 0% Gaps 0%

QY 1 MPEFIVYALIVVALVYIAKLVVPI 244; 100% coverage of the WT sequence
DB 1 MPEFIVYALIVVALVYIAKLVVPI 244; 100% coverage of the WT sequence
QY 61 AAYFSEFQNPIMMHHHFFRRH2ALFFVFAREH2ELZLFVAINVYHITZELCP 120
DB 61 AAYFSEFQNPIMMHHHFFRRH2ALFFVFAREH2ELZLFVAINVYHITZELCP 120

RESULT 14

AAV64672
ID AAY64672 standard; Protein: 115 AA;

XX AAY64672;

DE 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:844.

XX Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence;
KW torensin; location development; protein synthesis stability;
KW regulation; identification

XX Homo sapiens.

XX W09954051-A2.

XX 21-OCT-1999

XX 09-APR-1999; 99W0-1800712.

XX 09-APR-1998; 98W0-0557719.

XX 28-APR-1999; 98W0-0564047.

XX (GENSET) GENSET.

XX Thomas Milne Edwards J.; Lucifert A.; Lucifert B.

XX WPI: 2000-038446/03

XX N PSDB: AAY42286

XX Novel secreted protein; 5' expressed sequence tag sequences used in
PI diagnostic, torensin, gene therapy, and chromosome mapping products

XX claim 4; Page 604; 843pp; English.

XX AAY42266 to AAY43090 represent nucleic acid expressed sequence tags (ESTs)
CC sequences corresponding to human secreted proteins (AAY4266 to
CC AAY43090 represent the 3' related proteins corresponding to AAY4266 to
CC AAY43090). The 5' ESTs can be used for producing secreted human gene

[illegible]

RESULT 7
 US 08 916-576B-4
 ? Sequence 4, Application US/08916576R
 ? Patent No. 6171816
 ? GENERAL INFORMATION:
 ? APPLICANT: YU GUO-LIANG
 ? APPLICANT: GILLEN, PATRICK J.
 ? APPLICANT: EBER, REINHARD
 ? APPLICANT: EBER, REINHARD
 ? APPLICANT: EBER, REINHARD
 ? TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTOR
 ? NUMBER OF SEQUENCES: 45
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: STERN, KESSEL, GELFANT & CO., P.C.
 ? STREET: 1100 NEW YORK AVENUE, SUITE 600

```

1 COUNTRY: US
2 ZIP: 22005-4644
3
4 COMPUTER READABLE FORM:
5
6 MEDIUM TYPE: floppy disk
7
8 COMPUTER: IBM PC compatible
9
10 OPERATING SYSTEM: PC DOS/MS-DOS
11
12 SOFTWARE: Patent in Progress #1.0, Version #1.0
13
14 CURRENT APPLICATION DATA:
15
16 APPLICATION NUMBER: 11,100,916, 6/94

```

CLASSIFICATION: 536
PRIOR APPLICATION DATA: US 60/024,447
APPLICATION NUMBER: US 60/024,447
FILING DATE: 23 AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/CITATION NUMBER: 1489,059,001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:

Query Match	24.7%	Query Size	10	Length	171
Best Local Similarity	34.2%	Pred. No.	8,3018		

[illegible]

QY 134 SLFVPRADITGRYSNRUYAYEPAQFALLANMKKAKLL 171

14 1. TITLE: 3-AMINO-1,4,6-TRIMETHYLVARNOLINE
 2
 3 RESULT: 6
 4 99-09 994-681-6
 5 7 Sequence 6, Application 05/08884681
 6 Patent No. 055138
 7 8 GENERAL INFORMATION:
 9 9 APPLICANT: Hillman, Jennifer L.
 10 10 APPLICANT: Loh, Preseli
 11 11 APPLICANT: 415 855 0655
 12 12 APPLICANT: Shah, Purvi
 13 13 TITLE OF INVENTION: NEW HUMAN 1B-1B-BLATTEN-18-1
 14 14 NUMBER OF SEQUENCES: 1
 15 15 CORRESPONDENCE ADDRESS:
 16 16 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 17 17 STREET: 3174 Porter Drive
 18 18 CITY: Palo Alto
 19 19 STATE: CA
 20 20 COUNTRY: USA
 21 21 ZIP: 94304
 22 22 COMPUTER READABLE FORM:
 23 23 METHOD TYPE: Diskette
 24 24 COMPUTER: IBM compatible
 25 25 OPERATING SYSTEM: DOS
 26 26 SOFTWARE: PSEQU for Windows Version 2.00
 27 27 SOURCE APPLICATION DATA:
 28 28 APPLICATION NUMBER: 05/09/091-01
 29 29 FILING DATE: Filed herewith
 30 30 PRIOR APPLICATION DATA:
 31 31 APPLICATION NUMBER:
 32 32 FILING DATE:
 33 33 ATTORNEY/AGENT INFORMATION:
 34 34 NAME: Hillman, Lucy L.
 35 35 REGISTRATION NUMBER: 06,745
 36 36 REFERENCE NUMBER: 11-004 US
 37 37 TELECOMMUNICATION INFORMATION:
 38 38 TELEPHONE: 415 855 0655
 39 39 TELEFAX: 415 845 4166
 40 40 INFORMATION FOR SEQ ID NO: 5:
 41 41 SEQUENCE CHARACTERISTICS:
 42 42 LENGTH: 501 amino acids
 43 43 TYPE: amino acid
 44 44 STRANDNESS: single
 45 45 TOPOLOGY: linear
 46 46 IMMEDIATE SOURCE:
 47 47 LIBRARY: GenBank
 48 48 CLONE: 1420920
 49 49 05-08-884-681-5

Query Match	9.1%	Score 81.5	18.2	Length 901
Best Local Similarity	23.7%	Prod. No. 1.2		
Matches	45	Conservative	32	Mismatches 46
				Indels 67
				Gaps 18

[illegible]

US/09260043

INVENTOR: JAMES W. WILSON, JR.
ATTORNEY: JAMES W. WILSON, JR.
CLASS: 35/230.01
TITLE: NEW HUMAN PROTEIN...
ABSTRACT: A new human protein...

CLASS: 35/230.01
TITLE: NEW HUMAN PROTEIN...
ABSTRACT: A new human protein...

CLASS: 35/230.01
TITLE: NEW HUMAN PROTEIN...
ABSTRACT: A new human protein...

CLASS: 35/230.01
TITLE: NEW HUMAN PROTEIN...
ABSTRACT: A new human protein...

CLASS: 35/230.01
TITLE: NEW HUMAN PROTEIN...
ABSTRACT: A new human protein...

GENERAL INFORMATION:
APPLICANT: JAMES WILSON, JR.
INVENTOR: JAMES WILSON, JR.
TITLE: NEW HUMAN PROTEIN...
ABSTRACT: A new human protein...

Query Match:
Best Local Similarity: 25.7%
Matches: 453
Mismatches: 403
Inserts: 403
Deletions: 403
Substitutions: 403

RESULT: 11
US-09-418-54-007
Sequence 7, Applicant 10/18/98/ 418-54-007
Patent No. 6,240,240
GENERAL INFORMATION:
APPLICANT: JAMES WILSON, JR.
INVENTOR: JAMES WILSON, JR.

Q7 140 D1 ----- PPKYSNRLLYAYEFAU1 157
11 11 11 11 11
D6 410 D1 LLKAA1AAS3GVSE1VSAWASAS1 435

Search completed: July 18, 2002, 10:20:41
Job time: 122 sec

of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH_MGC library.

BASE COUNT 279 a 192 c 173 g 203 t
ORIGIN

Query Match 86.4%; Score 747.8; DB 10; Length 846;
Best Local Similarity 96.2%; Pred. No. 420-165;
Matches 786; Conservative 0; Mismatches 28; Indels 3; Gaps 2.

QY 44 qcaqftgggtgaqaaatccagagttgccatqagagaaattccagttccagcattcttgc 103
Db 11 GCGCGGCACTACACACAGGAGAGTGGCAATGGAGAAAAATCCAGTGTCCAGCATCTTGC 70
QY 104 tectttatggctctcccaactctggccagagatatacaaatccaaactctggcagaaa 163
Db 71 TCCTTGTGGGCTCTCTACACTCTGGCCAGAGATAGACAGTCAAACTGGAGCCAAAA 130
QY 164 agaacacaaagagactctcgaacaaactggccagagcctctccagagtttggagttgac 223
Db 131 AGCACACAAAGGACTCTCGACCCAAACTGCCCCAGAGCCCTCTCCAGAGTTGGGGTGACC 190
QY 224 aactcattctgaactcagacatatqagagagctctatatcaatccaaagcagcaaaac 283
Db 191 AACTCATCTGGACTCAGACATATGAAGAAGCTCTATATATAATCCAAAGACAGCAAAAC 250
QY 284 ccttgatgattattcattcactctgattgagttgagttgagttgagttgagttgagtt 343
Db 251 CCTGTGATGATTATTCATCCTTGATGATGATGATGATGATGATGATGATGATGATG 310
QY 344 tggctgaatataaagaaatccagagttggcagagagagagagagagagagagagagag 403
Db 311 TTGCTGAAATATAAGAAATCCAGAAATGGCAGAGCAGTTGTCTCTCTCTCTCTCTCT 370
QY 404 atgaacaaactgaacaaac 463
Db 371 ATGAACAACTGACAAACACCTTCTCTCTGATGGCCAGTATGTCCTGAGGATTATGTTG 430
QY 464 ttgacccattctctgacagttaagagccgatatcactggaagatatccaaacacacacac 523
Db 431 TTGACCCATTCTTGACAGTTAGAGCCGATATCAGTGAAGATATTCAAAGGCTCTATG 490
QY 524 cttaagaaactcagacatatcagagtttgttgaatgaacacacacacacacacacacac 583
Db 491 CTTACGAACCTGACATACAGCTCTGTTGCTTGACAGATGAGAAAGCTCTCAAGTTGC 550
QY 584 tgaagactgaattgttaagaaacacacacacacacacacacacacacacacacacacac 643
Db 551 TGAAAGACTGAATTGTAAAGAAACAAACAAATCTCCAAAGCCCTTCGTCGTCAGGCTTGAGA 610
QY 644 cttaagaaac 703
Db 611 CTTGAACCCAGAACAAAGTGTGAGAAAGACTGGCTAGTGTGGAAAGCATAGTGAACACACTGA 670
QY 704 ttaqgttatgttttaattgtac 762
Db 671 TTAGGTGATGGTGTAAATGTTACAAACAACTATTTTAAAGAAACAAACAAAGTTTAAAGAAAT 730
QY 763 tgggtttcaagtgtacatgtgtgaacacacacacacacacacacacacacacacacacac 822
Db 731 GGGTTTCAAGTGTACATGTGTGAAAG-ATATGGTATACATACCATAGTGGCCATGAAT 789
QY 823 tctaaaaaaataaataatgttttggggtgttctcttctctc 865
Db 790 TCTAAACAAACAAATCAGCGGTAGCGGGGTGTACAGGACACTC 832

RESULT 2
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LOCUS
DEFINITION 601580166F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942112 5',
mRNA sequence.

BE796856
BE796856.1 GI:10218156
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFLENGTH 1 (bases from 1 to 948)
TITLE NIH_MGC_7: cDNA clone image
Nucleotide collection (GenBank, Human) and cDNA clones (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DBP
cDNA Library Preparation: Linda Hanrahan/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LCM795 row: d column: 17
High quality sequence stop: 748.
FEATURES
Location/Qualifiers
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/organism "Homo sapiens"
/db_xref="taxon:9606"
/clone "IMAGE:3942112"
/cfeature_lib "NIH_MGC_7"
/feature_type "small cell carcinoma"
/cell_line "MGC3"
/lab_host "DH10B (phage-resistant)"
/note "Origin: Insert: Vector: pDR7; Site: 1; XhoI; Site: 2;
XhoI; cDNA made by oligo dT priming. Directly
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Size-selected (500bp) for average
insert size 1.8kb. Library constructed by ligation in
the laboratory of Gerald H. Rubin (University of
California, Berkeley) using ZAP cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 296 a 225 c 207 g 220 t
ORIGIN

Query Match 86.2%; Score 746.2; DB 10; Length 948;
Best Local Similarity 96.2%; Pred. No. 420-165;
Matches 786; Conservative 0; Mismatches 28; Indels 3; Gaps 2.

QY 35 tcaacacaaagcaggttgggtgaqaaatccagagttgccatgaagaaatccagagttgc 94
Db 1 TCACACAAAGGAGAGTGGGTGAGGAAATTCAGAGTTGGTATGGAGAAAAATCCAGTGTGAG 60
QY 95 cacttcttgcctcttgcctctcctcactcctcagcagagagagagagagagagagagag 154
Db 61 CATTCTGTCTCTGTGGCCCTCTCTCTACTCTCTGGCAGAGATAGCAGTAAATCTG 120
QY 155 agagcctaaagaaagaaagcagcagagagagagagagagagagagagagagagagag 214
Db 121 GAGCCAAAAAGGAG 180
QY 215 ggggtgac 274
Db 181 GGGGTGACCAACTTATCTGGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 275 gcaac 334
Db 241 GCAACAAAAAGGAG 300
QY 335 ag 394
Db 301 AGAAAGGTGTGGTGAAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460
QY 395 gacttgaatttatgaag 454
Db 361 ATCTGGTTTATGAAAGAAATGAGAAAAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420

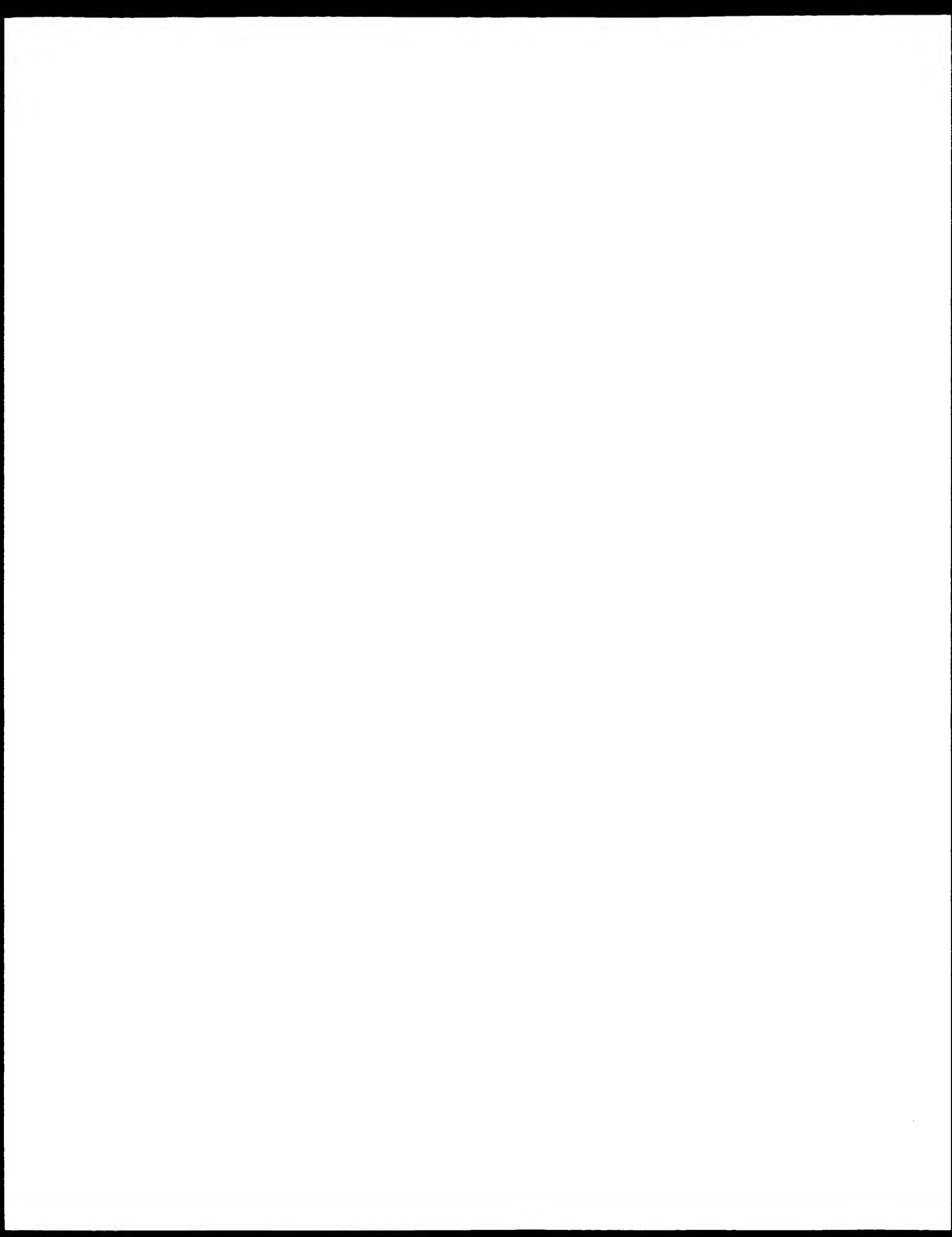


Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.



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1 1 NAME:
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Query Match:
Result:
Matches:
1 1 NAME:
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7 1 FAX:
8 1 EMAIL:
9 1 COMMENTS:
10 1
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12 1
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5 1 ZIP:
6 1 PHONE:
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8 1 EMAIL:
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[illegible]

RESULT 15
 US 09 828 792-923
 1. INVENTOR: GILBERT, DAVID P.
 2. GENERAL INFORMATION:
 3. APPLICANT: GILBERT, DAVID P.
 4. APPLICANT: ROBINSON, KEITH E.
 5. APPLICANT: HOLTSMAN, DONALD A.
 6. TITLE OF INVENTION: Nucleic Acid Molecules
 7. TITLE OF INVENTION: Human Fetal Tissue Like
 8. FILE REFERENCE NUMBER: 34Pa
 9. CURRENT APPLICATION NUMBER: 09/092,872
 10. CURRENT FILING DATE: 2001-04-19
 11. PRIOR APPLICATION NUMBER: 09/092,872
 12. PRIOR FILING DATE: 1999-06-11
 13. PRIOR APPLICATION NUMBER: 09/092,872
 14. NUMBER OF SEQ ID NOS: 102
 15. NUMBER OF SEQ ID NOS: 102
 16. SUMMARY: Particulate Virus-Like Virus-Like
 17. SEQ ID NO: 923
 18. LENGTH: 173
 19. TYPE: PR1
 20. FEATURE:
 21. FEATURE:
 22. LOCATION: (1) ... (20)
 23. 09 029 792-923



US-09-793-4409-4

THE UNIVERSITY OF CHICAGO

61 ALVFFNFFLMTTHLCTTHVAAFEVTVZNNKELFLBGLVLRHLYVLTTHGHHH 120

2009-10-27 10:10:10

THEORY

ORGANISM: Homo sapiens

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[illegible][illegible]

THE (6) (7)

LEWIS, R. L.

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[illegible]

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TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..900
OTHER INFORMATION: Ceres Seq. ID no. 3034209
US 09-935-625-25975

Query Match 9.3% Score 83.5; DB 5; Length 900;
Best Local Similarity 21.3% Pred. No. 8.6;
Matches 46; Conservative 41; Mismatches 76; Indels 53; Gaps 9;
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DB 80 PQSQUILLFESSYSLOTTPSSRYKTSIQNFKEFIASISQSEFQPR SEAFESQPELS 137
QY 56 QTYPPKAYVPEPTGHEFLM- - - - -LHQLFQTHLQALFFVVAQNFEEICFLAEQVLL- - - 107
DB 148 EAEIVVVEREIVVGEVLLGLHEITTEGCTTHLQ ELVNNLELQTHREHIVGQDIN 194
QY 108 - - - - -NIAYETTHKHSPLQGVPR - - - - -IMFVPSLTVRADL- - - 141
DB 195 HVNPIESTVAHSLTESQGL- - - - -STVSSITPRSSQSEELGRIIVGIVGDDIKRISTSEL 251
QY 142 - - - - -PGPYNNELVAYELADTALLLNPKKALKKELTEL 175
DB 242 HESQIRKQKAVVWQSAEYVTHNLRKREKFEELKMRKAL 290

Search completed: July 18, 2002, 10:23:26
Job time: 217 sec


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Best Local Similarity 23.9% Prod. No. 4.23
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111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 40 WTQV KKKAAKPTPTPTTMTTHRLKSLKELALEPVTATREELKMAELINLKKVETET 88
111 111 111 111 111 111 111 111 111 111 111 111 111
07 114 TDKHLSPDQY-----VPRIMKVIDSLTVR 138
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DB 89 FURNLHLKQAYGPTIQKGFPAVVVVNSLKKVR 120
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Search completed: July 18, 2002, 10:21:05
Job time: 126 sec

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10b	122	KYVAMVICHITETRA	QVAMAGNETIKAL	SEIVIV			IKMESANINDEPV	175
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Q7	130	FVPISTIVKADIT	QVYSNIVAYE	PAIADILENNEK	KALKER		172	
		111	111	111	111	111	111	
10b	176	-----	ADLEKRWAMVIL	TERDOPM	TAULIDWAK	IRLE	210	
		111	111	111	111	111	111	

[illegible]

Class I peptidase (EC 3.4.11.1) (Carboxypeptidase

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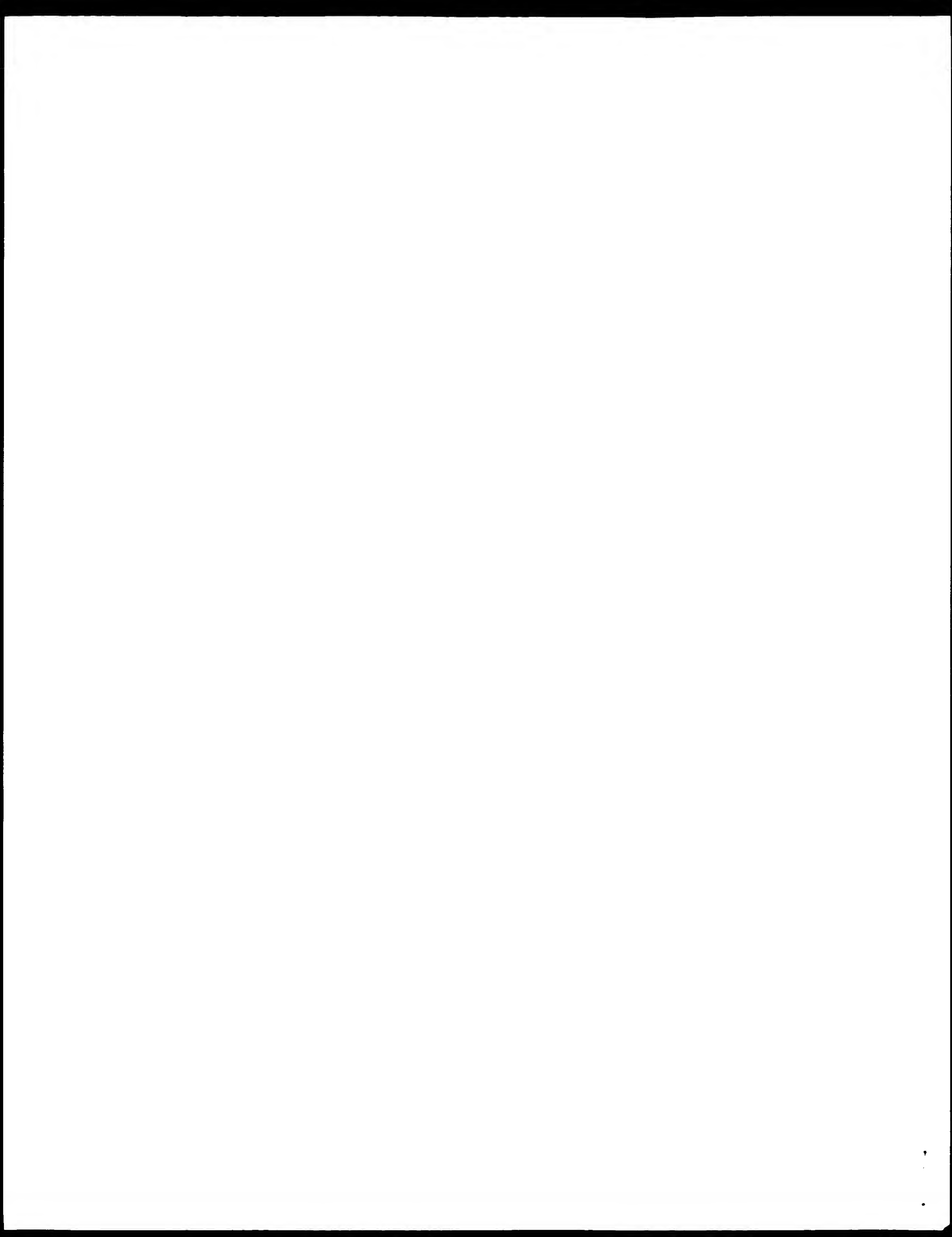
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[illegible]

[illegible]

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DI	01-JUN-2001 (EMBLrel. 17, Last sequence update)
DE	01-JUN-2001 (EMBLrel. 17, Last annotation update)
DE	HYDROPHILIN 14.2 kDa protein.
GN	FLK16.21
OC	Archaea; Eukarya; (House-eat cross)
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC	Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosales
OC	eurosid 11; Brassicales; Brassicaceae; Arabidopsis.
OX	SwissProt:37025
RN	111
RF	SWISSPROT:37025
RC	STRAIN CV, COLUMBIA
EX	MEDLINE:210719; PubMed-11137127
RA	Theologis A, Becker J.R., Palm G.J., Federspiel N.A., Kaul S.,
RA	Witt C., Zeng L., Zeng B., Araric P., Beckman J., Brooks S.Y.,
RA	Buchler E., Chan A., Chao Q., Chen H., Chen K., Chin C.W.,
RA	Chen M., Chen Y., Chow A.H., Conway P., Fowler K.,
RA	Dunn P., Elgu P., Feldblum T.V., Fong J., Fong P., Fung Y.,
RA	Gill J.E., Goldsmith A.D., Hais K., Hansen N.P., Hughes K., Hunter J.,
RA	Hunter J.L., Jenkins J., Johnson Boppre J., Khan S., Khaykin B.,
RA	Kim S., Koo H., Kravtsovskiy I., Kuznetsov K., Lam K.,

